

117: qb_08148:*

118: qb_08149:*

119: qb_08150:*

120: qb_08151:*

121: qb_08152:*

122: qb_08153:*

123: qb_08154:*

124: qb_08155:*

125: qb_08156:*

126: qb_08157:*

127: qb_08158:*

128: qb_08159:*

129: qb_08160:*

130: qb_08161:*

131: qb_08162:*

132: qb_08163:*

133: qb_08164:*

134: qb_08165:*

135: qb_08166:*

136: qb_08167:*

137: qb_08168:*

138: qb_08169:*

139: qb_08170:*

140: qb_08171:*

141: qb_08172:*

142: qb_08173:*

143: qb_08174:*

144: qb_08175:*

145: qb_08176:*

146: qb_08177:*

147: qb_08178:*

148: qb_08179:*

149: qb_08180:*

150: qb_08181:*

151: qb_08182:*

152: qb_08183:*

153: qb_08184:*

154: qb_08185:*

155: qb_08186:*

156: qb_08187:*

157: qb_08188:*

158: qb_08189:*

159: qb_08190:*

160: qb_08191:*

161: qb_08192:*

162: qb_08193:*

163: qb_08194:*

164: qb_08195:*

165: qb_08196:*

166: qb_08197:*

167: qb_08198:*

168: qb_08199:*

169: qb_08200:*

170: qb_08201:*

171: qb_08202:*

172: qb_08203:*

173: qb_08204:*

174: qb_08205:*

175: qb_08206:*

176: qb_08207:*

177: qb_08208:*

178: qb_08209:*

179: qb_08210:*

180: qb_08211:*

181: qb_08212:*

182: qb_08213:*

183: qb_08214:*

184: qb_08215:*

185: qb_08216:*

186: qb_08217:*

187: qb_08218:*

188: qb_08219:*

189: qb_08220:*

190: qb_08221:*

191: qb_08222:*

192: qb_08223:*

193: qb_08224:*

194: qb_08225:*

195: qb_08226:*

196: qb_08227:*

197: qb_08228:*

198: qb_08229:*

199: qb_08230:*

200: qb_08231:*

201: qb_08232:*

202: qb_08233:*

203: qb_08234:*

204: qb_08235:*

205: qb_08236:*

206: qb_08237:*

207: qb_08238:*

208: qb_08239:*

209: qb_08240:*

210: qb_08241:*

211: qb_08242:*

212: qb_08243:*

213: qb_08244:*

214: qb_08245:*

215: qb_08246:*

216: qb_08247:*

217: qb_08248:*

218: qb_08249:*

219: qb_08250:*

220: qb_08251:*

221: qb_08252:*

222: qb_08253:*

223: qb_08254:*

224: qb_08255:*

225: qb_08256:*

226: qb_08257:*

227: qb_08258:*

228: qb_08259:*

229: qb_08260:*

230: qb_08261:*

231: qb_08262:*

232: qb_08263:*

233: qb_08264:*

234: qb_08265:*

235: qb_08266:*

236: qb_08267:*

237: qb_08268:*

238: qb_08269:*

239: qb_08270:*

240: qb_08271:*

241: qb_08272:*

242: qb_08273:*

243: qb_08274:*

244: qb_08275:*

245: qb_08276:*

246: qb_08277:*

247: qb_08278:*

248: qb_08279:*

249: qb_08280:*

250: qb_08281:*

251: qb_08282:*

252: qb_08283:*

253: qb_08284:*

254: qb_08285:*

255: qb_08286:*

256: qb_08287:*

257: qb_08288:*

258: qb_08289:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

[illegible][illegible]

Db 1 GACCGAGAGTGTGACCATGACAAAGTGAAGAGCTCCAGTGTGTGTGGAGAGGCACTTACA 60
 QY 537 acagagccctcttagagcatctacagcgaagaaataatctacgtctcgttgaagttc 596
 Db 61 ACAGAGCCCTCTTAGACAAATTAATATGCAAGAGCAAAATTAACCTCCGCTGACGGCTT 120
 QY 597 tccgcgtcgaagaatacatcttgaacatcttgaagagatcttgaacgtctcgttaaacg 656
 Db 121 TCGGCTCGGCAAGATACATTAATGACATTAAGTCTGACGAGCTTCTTAACCTCTGTAATAGC 180
 QY 657 actctatgatttgcacacagatcatcttcttaacatcagtgagcagcgtctccagatgc 716
 Db 181 ACCTCATGTTGTGACCCAGCCGATCATCTTTATATCATGTAGATGATGTCTCCAGCATGC 240
 QY 717 ctctgataagagcttgcgcctcgtcgtcccttcaaaagcttctgagtgatcaacccagagga 776
 Db 241 CTGTGATAGAGTTGGTCCCTGCTGCTGCTTCACAAAGCTTTAATATCAACCTGACAGAGA 300
 QY 777 gctgcagagagcttgcagatcgtcagatcgaagacatcggggaagacatcgtgagccaca 836
 Db 301 GGTGCGAGCAGATCAGCATATAGCATGCAAGACTATCGGCGACACATGTGCGCCACACA 360
 QY 837 tccagcgtgagatgagatctctcttctcagatgagcgtgagcaggtcttccaaagcagat 896
 Db 361 TCCAGCATGAGAGTTGATCTCTTTTTCATGAGATGTGACGACAGCTCTTCCAAAGACAGT 420
 QY 897 tccagcgtgagagacccctggttgaatcagtcagtcagtcagtcagtcagtcagtcagtcag 956
 Db 421 TTGGGCTGGAGACCTCTGCGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
 QY 957 atcccgatgagtt 969
 Db 481 ATCCCATGACCTT 493

RESULT 6
 AM463741 479 bp mRNA EST 24-FEB-2000
 LOCUS BP230013810C8 5', mRNA sequence.
 DEFINITION
 ACCESSION AM463741
 VERSION AM463741.1 GI:7033909
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 479)
 AUTHORS Lewin,H.A., Soares,M.B., Rehbeiz,M., Pardinas,J., Liu,L. and Larson,
 J.D.H.
 TITLE Bovine ESTs
 JOURNAL Unpublished (2000)
 COMMENT W. M. Keck Center for Comparative and Functional Genomics
 University of Illinois at Urbana-Champaign
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
 61801, USA
 Tel: 217 333 5998
 Fax: 217 244 5617
 Email: h-lewin@uiuc.edu
 Funding for cattle EST sequencing was provided by the USDA National
 Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
 from Washington University Genome Center. Vector Trimmi g:
 Cross-match from Washington University Genome Center PHRAP suite.
 Sequences submitted are vector free and at least 200 bp in length.
 PCR PRIMERS
 FORWARD: TAAATGACATGACTATAGCG
 BACKWARD: ATTATGCTGACTAAG
 Insert Length: 479 Std Error: 0.00
 Plate: BP230013810 row: G column: 8
 Seq primer: AGCGATACAAATTTACACAGCA

FEATURES High quality sequence stop: 479.
 Location/Qualifiers
 source 1..479
 /organism="Bos taurus"
 /db_xref="taxon:9913"
 /clone_lib="BP230013810G8"
 /clone_lib="Soares normalized bovine placenta"
 /sex="female"
 /lab_host="DH10H"
 /note="Organ: Placenta; Vector: pTZ193; Site_1: Prok1;
 Site_2: Not1; The cDNA library was constructed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lembo, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806."

HASH COUNT 142 a 102 c 122 g 113 t
 ORIGIN

Query Match 32.6%; Score 424.4; DB 116; Length 479;
 Best local similarity 94.0%; Pred. No. 6,9e-108;
 Matches 453; Conservative 0; Mismatches 26; Indels 4; Gaps 1;
 QY 270 acagcccaagagcctcttcttctgataacccatcaaaagcccaagatcagatgagc 429
 Db 1 ACAGCCCAAGAGCCTCTTGTGTGATTAAGCCATCAAAAGCCAGAGT---TGCTG 57
 QY 330 gcaagcagatctcgaagagcttgaatggttccagatgatttaacaaatgattacaaag 389
 Db 58 GCAGCAGCATTCAGAGAGGCTGCTGCTTCCGAGATGCTTTAACAAATGATTAACATGAA 117
 QY 390 aaatgaaagcgttaagcgaagaaagaaagaaagaaagaaagaaagaaagaaagaaag 449
 Db 118 AAGATGAGCATTAAGCAGAGAAAGCAAGCAAAACCAAGACCAAGAAATAGCTTAAGT 177
 QY 450 tatcgaactggttcaacccatttaacgccttgaagttgattgattgattgattgattgatt 509
 Db 178 TATCGAGCTGCTTCACCCATTAAAGCCCGGAGGCTTGATGATGATGATGATGATGATGATG 237
 QY 510 caccggtggttgaagagagcattacaaatgagagcgtcttaagatgattacacacacac 569
 Db 238 CTCAGTGTGCTGGAGAGGCTTACACAGACAGCCGCTTACCAATTATATAGCCAAAG 297
 QY 570 aaaaattac 629
 Db 298 ACAAAATTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 357
 QY 630 agagatcttaagctcgtcctaataagcattcagttgagcagcagcagcagcagcagcag 689
 Db 358 AGAGTCTTAAGCTGCTGCTAATAAGACTTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 417
 QY 690 tcatgtgagagagcgtctccagagatgcttgaatgagatgagatgagatgagatgagat 749
 Db 418 TCAATGATAGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477
 QY 750 aa 751
 Db 478 AA 479

RESULT 7
 AM464433 475 bp mRNA EST 24-FEB-2000
 LOCUS BP230013820C5 5', mRNA sequence.
 DEFINITION
 ACCESSION AM464433
 VERSION AM464433.1 GI:7034601
 KEYWORDS EST.
 SOURCE
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovidae; Bovinae; Bos.
 REFERENCE 1 (bases 1 to 475)

DB 223 CAAAGCTATTAATCTTAATCCCGGAATACCTCGTGAGTATATACATAGAGCTTACCTTC 164

UY 1237 ggaatattacgtctgcacgaatctcttcgacacacaaagatataatgctttagaataat 1296

DB 163 GGATTTATAGCTTCACAGATGTTCTTGCCAGACAAAGAGTATATGTTGATGAATAA 104

UY 1297 catctga 1303

DB 103 TGTCTGCA 97

RESULT 9

AKO15047

LOCUS

DEFINITION

AKO15047

AKO15047.1 GI:12853236

VERSION

KEYWORDS

SOURCE

Mus musculus (strain:J57H/6u) adult male testis cDNA to mRNA, clone J1bRIKEN full-length enriched mouse cDNA library

clone:49-0402F0b.

Mus musculus

Ennariotia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ORGANISM

REFERENCE

1 (sites)

Carninci, P., and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Methods Enzymol. 303, 19-44 (1999)

2 (sites)

Carninci, P., Shibata, Y., Hayatsu, N., Sunahara, Y., Shibata, K., Itoh, M., Komuro, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

MEDLINE

20499374

3 (sites)

Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Kituchin, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Iwama, M., Ohara, E., Matsuda, K., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Okazaki, Y., Muramatsu, M., Inoue, Y., and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipicillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

MEDLINE

20530913

4 (sites)

The RIKEN Genome Exploration Research Group Phase II Team and FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 685-690 (2001)

5 (bases 1 to 1370)

Aachil, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arikawa, T., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Haragaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Iwama, M., Kato, H., Kawai, J., Kojima, Y., Komuro, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shingagawa, A., Shiraki, T., Soabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, Y., Tejima, Y., Toyai, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: genome-res-qsc.riken.go.jp, URL: http://genome.usc.riken.go.jp/, Tel: 81-45-503-9222).

TITLE

JOURNAL

COMMENT

Fax:81-45-503-9216)
Please visit our web site (<http://genome.asc.tken.ac.jp/>) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5'-GACATAGAAACAGATTCCACAGACTCTTTTITTTTTTN 3'}. cDNA was prepared by using triethanolamine-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Ret = 10.0 and subtraction to Ret = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5'-

GACAGAGACTTCCTCAGCTTAATTAATTAATCGGGCCCC 3'}. cDNA was cleaved with BamHI and XhoI. Vector: a modified phage-script KS(-) after bulk excision from Lambda F10. Cloning sites: 5' end: SalI; 3' end: BamHI. Host: DH10B.

FEATURES

source
location/qualifiers
1..1370
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="MG:MGI:1908146"
/db_xref="MG:MGI:1922104"
/clone="4930402P06"
/sex="male"
/tissue_type="testis"
/clone_id="Riken_full-length enriched mouse cDNA library"
/dev_stage="adult"

BASE COUNT
407 a 286 c 299 g 378 t

ORIGIN

```

Query Match      29.6%; Score 385.2; DB 192; Length 1370;
Best Local Similarity 69.6%; Pred.No. 9,4e+97;
Matches 536; Conservative 0; Mismatches 233; Indels 1; Gaps 1

```

OY	523	ggaagacattacaacagaagcgcctcttaagactactaacgcaacgaaataccgt	582
Dd	495	ggcacacaccttcacatgacttagtttgccagattattaiagacacatcccatcggt	554
OY	583	cgcctcgaagctlltcgcgcgcgcgaagatagactlaagactltaaggaaattcctaac	642
Dd	555	-ggtagatccgtggttgcagtgagggagagatgcccttttgactcctgggtacg	613
OY	643	gtctcgaataagacacttatggttgcgcgcgcgaagatcattltaagatgatgaaga	702
Dd	614	atcgcgcgactagcttcttcatagttaaacacgaagctcattttacatcatctgtacga	673
OY	703	cgctccgaagatgcctttaagadagctgggcctctcgagctcctccaagatattgaat	762
Dd	674	ctttctcctaatgcccattgcctgacatctgacgtccgcaatcgacataaagatcttaacat	733
OY	763	caagcctgaagaaagatgcgcgaagatgcgaatgatatgcatalgaagaacatcgaagaag	822
Dd	734	tAACCAAGCGCGTAGGTGCAGAATAATCGCATATGTCGCAATGAACCTTCAAGTGACA	793
OY	821	catctgtgcgcgaatccagacatgaagctgaagctacctcttctgaatgaagctgaagcgaat	882
Dd	794	CATCGAGGTCACTACATACACATAGAGAGTTTACTATATGCTCTGTGATGCAATGTGATTAAT	853
OY	883	cttccgaagcgaattcgaggatgaagacctggagtgagtcgaagcgcgaatccaaagctga	942
Dd	854	ATTCAAAGCGAAGTACGGTCTGTGACAGCTCTGGAGAGCTCTGTAGCTCACGTGCAATGATA	913
OY	943	gtggtacaagcgaatcccaatgaatttaactiaagaaagacgaaggaagatctgaagata	1002
Dd	914	TTCGTACAAGCAAGATCGCAGCAAAATACCTTATGCAAGAAATCAATCAATCAAGAACTGA	973
OY	1003	catctcccttcgagcgaaggaattttatatacgaagacgaatctttgaagaaacacac	1062
Dd	974	CATACGATGAGCGAGGGGAGACTTTTATTACCATGCTGTGTTTGTTTTGAGGGACAAAGCCAC	1033


```

QY 431 gacaaagaaagccttaagatcagactggtcctcaacccattaaagccctgaagttctg 490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 160 cgcatttgaaagacacctagctatgagagctgttcaacaaagacccggatgtttg 219
QY 491 actaatgagatgaagagacccggtggttgggaaggaacttaacagagccgtctta 550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 220 acagtgaccccgtagaagccggccatgtgttggaagagactttatgacacacactgtctg 279
QY 551 gacgattactaacgcaagagaanaatfacgctgagctgaagcttctgcctcgaaga 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 280 gaaatattaccacccacacagaaactcgttgggcctgcacgtgtgtgttggaag 339
QY 611 taacttgacatctacttggagagatcttctaaacgtctgtaataagcaacttcagttgac 670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 340 tgcattgacattacttaacagacatttgcagctgctgacatgacttcatgtgtgac 399
QY 671 gacgaatcacttcttcaatgagagagagctctcctcgaatgacttcttgaagagctg 730
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 400 cagcgggtatatttttactcctatgatacagacactctccgagatgctgtgacactg 459
QY 731 ggcctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 790
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 460 aacccctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 519
QY 791 agcagtgatgagatgaagacacacacacacacacacacacacacacacacacacacac 850
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 520 accatgagatgagatgaagacacacacacacacacacacacacacacacacacacacac 579
QY 851 gacgctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 580 gacttcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 639
QY 911 ctgggtgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatg 970
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 640 ctgggtgagatgagatgagatgagatgagatgagatgagatgagatgagatgagatg 699
QY 971 accta 975
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 700 accta 704

```

```

RESULT 12
AV666881/ 399 bp mRNA EST 25-AUG-2000
LOCUS AV666881 Bos laurus adipocyte cell line Bos laurus cDNA clone
DEFINITION E1AD021G06 3', mRNA sequence.
ACCESSION AV666881
VERSION AV666881.1 GI:9925911
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos laurus
            Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 399)
            Sugimoto, Y., Hirotsune, S., Takasuga, A., Itoh, R., Jitohzono, A. and
            Suzuki, H.
            bovine cDNA sequencing
            Unpublished (2000)
            Contact: Yoshikazu Sugimoto
            Animal Genetics Division
            Shitakawa Institute of Animal Genetics
            Odakura, Nishigo, Nishi-Shitakawa, Fukushima 961-8061, Japan
            Tel: 81-248-25-5641
            Fax: 81-248-25-5725
            Email: kazusugi@acocoa.ocn.ne.jp
            Single pass sequencing.
            This clone was obtained from a polyA-deleted cDNA library.
            Location/Qualifiers
                1..399
                /organism="Bos laurus"
                /db_xref="taxon:9913"
                /clone="E1AD021G06"

```

```

FEATURES
    source
        1..399
        /organism="Bos laurus"
        /db_xref="taxon:9913"
        /clone="E1AD021G06"

```

```

/cldone_11b="Bos laurus adipocyte cell line"
/cell_type="an adipocyte cell line"
/lab_host="DH108"
/Note="Vector: pGL1; Site 1: SalI; Site 2: NotI; Poly A
was deleted from a NotI site"
BASE COUNT 102 a 113 c 89 g 95 t
ORIGIN
Query Match 25.5%: Score 331.8; DB 32; Length 899;
Best Local Similarity 92.7%; Prev. No. 5,88-82;
Matches 370; Conservative 0; Mismatches 27; Indels 2; Gaps 2;
QY 592 gatttcgacgacggaagataacattgaacatctacttgaagaaatcttcaagctctca 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 399 gctttgcgcctcgagaaatatacttgcacattacttgcagacattcttgcagctgcta 340
QY 651 ataagacattcagatgttgagcagcagcagcagcagcagcagcagcagcagcagcagc 709
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 339 ATAAGCAGCTTCATGCTGCGACCCACATCATTATATATGATGATGATGATGATGATG 280
QY 710 aggaatgcttgaatgaagatgagcctctgacgctcctcctcctcctcctcctcctcct 769
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 279 AGGATGCCCTTGATAGACTTGGTCTCTGCGCTCTCTCAAGCTTTAATATCAAGCC 220
QY 770 gaggagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 829
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 219 GAGAGAGAGTGGACAGATGAGATGATGAGATGAGATGAGATGAGATGAGATGAGATG 160
QY 839 gccacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 889
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 159 gccacacacacacacacacacacacacacacacacacacacacacacacacacacac 100
QY 890 gacgagctcggggtggaagcctgagtgagtgagtgagtgagtgagtgagtgagtgagtg 949
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 99 GACAGAGTTGGGGTGGACACCCGCCGACGTCGGTCCCACTAGACAGCTTCGGTGA 40
QY 950 aagcagatcccgatgagttacttacttacttacttacttacttacttacttacttact 988
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 39 AAGGCAGATCCCATGACTTCACCTACGACGAGGCGGAG 1

```

```

RESULT 13
BF042944 362 bp mRNA EST 10-MAY-2000
LOCUS BF042944
DEFINITION BP250002A10F3 Soares normalized bovine placenta Bos laurus cDNA
ACCESSION BF042944
VERSION BF042944.1 GI:10759999
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos laurus
            Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovidae; Bovinae; Bos.
            1 (bases 1 to 362)
            Lewin, H.A., Soares, M.B., Reibel, M., Pardinas, J., Liu, L. and Larson
            J.H.
            Bovine ESTs
            Unpublished (2000)
            Contact: Lewin, H. A.
            W. M. Keck Center for Comparative and Functional Genomics
            University of Illinois at Urbana-Champaign
            340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
            61801, USA
            Tel: 217 333 5998
            Fax: 217 244 5617
            Email: h-lewin@uiuc.edu
            Funding for cattle EST sequencing was provided by the USDA National
            Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
            to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
            from Washington University Genome Center. Vector Trimmi g:
            Cross-match from Washington University Genome Center PHRAP suite.

```

```

REFERENCE
    AUTHORS
        Lewin, H.A., Soares, M.B., Reibel, M., Pardinas, J., Liu, L. and Larson
        J.H.
    TITLE
        Bovine ESTs
    JOURNAL
        Unpublished (2000)
    COMMENT
        Contact: Lewin, H. A.
        W. M. Keck Center for Comparative and Functional Genomics
        University of Illinois at Urbana-Champaign
        340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
        61801, USA
        Tel: 217 333 5998
        Fax: 217 244 5617
        Email: h-lewin@uiuc.edu

```

```

FEATURES
    source
        1..362
        /organism="Bos laurus"
        /db_xref="taxon:9913"
        /clone="BF042944"

```


